



Multiple Imputation with Diagnostics (mi) in R: Opening Windows into the Black Box

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Abstract

Our **mi** package in R has several features that allow the user to get inside the imputation process and evaluate the reasonableness of the resulting models and imputations. These features include: choice of predictors, models, and transformations for chained imputation models; standard and binned residual plots for checking the fit of the conditional distributions used for imputation; and plots for comparing the distributions of observed and imputed data. In addition, we use Bayesian models and weakly informative prior distributions to construct more stable estimates of imputation models. Our goal is to have a demonstration package that (a) avoids many of the practical problems that arise with existing multivariate imputation programs, and (b) demonstrates state-of-the-art diagnostics that can be applied more generally and can be incorporated into the software of others.

Keywords: multiple imputation, model diagnostics, chained equations, weakly informative prior, **mi**, R.

1. Introduction

The general statistical theory and framework for managing missing information has been well developed since [Rubin \(1987\)](#) published his pioneering treatment of multiple imputation methods for nonresponse in surveys. Several software packages have been developed to implement these methods to deal with incomplete datasets. However, each of these imputation packages is, to a certain degree, a black box, and the user must trust the imputation procedure without much control over what goes into it and without much understanding of what comes out.

Model checking and other diagnostics are generally an important part of any statistical procedure. Examining the implications of imputations is particularly important because of the inherent tension of multiple imputation: that the model used for the imputations is not in general the same as the model used for the analysis (Meng 1994; Fay 1996; Robins and Wang 2000). We have created an open-ended, open source **mi** package, not only to solve these imputation problems, but also to develop and implement new ideas in modeling and model checking.

Our **mi** package in R (R Development Core Team 2011) has several features that allow the user to get inside the imputation process and evaluate the reasonableness of the resulting model and imputations. These features include: choice of predictors, models, and transformations for chained imputation models; standard and binned residual plots for checking the fit of the conditional distributions used for imputation; and plots for comparing the distributions of observed and imputed data. **mi** uses an algorithm known as a chained equation approach (Buuren and Groothuis-Oudshoorn 2011; Raghunathan, Lepkowski, Van Hoewyk, and Solenberger 2001); the user specifies the conditional distribution of each variable with missing values conditioned on other variables in the data, and the imputation algorithm sequentially iterates through the variables to impute the missing values using the specified models.

We omit a description of the theoretical background of multiple imputation since this material is available from many other sources (e.g., Little and Rubin (2002); Gelman and Hill (2007, chapter 25)). Rather, the major goal is to demonstrate the flexible way in which users can perform multiple imputation with **mi** and to introduce functions for diagnostics after imputation. The paper proceeds as follows: In Section 2, we provide an overview of steps to perform sensible multiple imputation. In Section 3, we demonstrate some novel features and functions of **mi** that address some imputation problems that have been neglected by other software. These features include: (1) Bayesian regression models to address problems with separation; (2) imputation steps that deal with semi-continuous data; (3) modeling strategies that handle issues of perfect correlation and structural correlation; (4) functions that check the convergence of the imputations; and (5) plotting functions that visually check the imputation models. In Section 4, we demonstrate how to apply these functions using an example of a study of people living with HIV in New York City (Messerli, Lee, Abramson, Aidala, Chiasson, and Jessop 2003). In Section 5, we discuss future plans for our **mi** package. The package is available from the Comprehensive R Archive Network at <http://CRAN.R-project.org/package=mi>.

2. Basic setup

The procedure to obtain sensible multiply imputed datasets approach requires four steps: setup, imputation, analysis, and validation. Each step is divided into substeps as follows:

1. Setup.

- Display of missing data patterns.
- Identifying structural problems in the data and preprocessing.
- Specifying the conditional models.

2. Imputation.

- Iterative imputation based on the conditional model.

- Checking the fit of conditional models and checking to see if the imputed values are reasonable.
 - Checking the convergence of the procedure.
3. Analysis.
- Obtaining completed data.
 - Pooling the complete case analysis on multiply imputed datasets.
4. Validation.
- Sensitivity analysis.
 - Cross validation.
 - Compatibility check.

At first glance, it may seem more complicated to conduct multiple imputation using **mi** compared to other available imputation software. However this is because we outline steps that other packages have traditionally ignored. **mi** is designed for both novice and experienced users. For the novice users, **mi** has a step-by-step interactive interface where users choose options from the given multiple choices and a graphical user interface (GUI) where users click buttons (see Section 4). For more experienced users, **mi** has simple commands that users can use to conduct a multiple imputation. This section simply describes the core functions. In Section 4, we will demonstrate how users can easily implement these imputation steps using **mi** via an example.

The implementation of the **mi** package is straightforward. The core function is a generic function `mi(object, ...)` which executes one of three methods depending on whether the input is a `data.frame`, or of S4 class `mi.preprocessed`, or `mi`. The `mi.preprocessed` class defines the output return by `mi.preprocess()` when it recodes special variables in a dataset (see Section 2 and Section 3). The `mi` class defines the output returned by `mi()` when it finishes a multiple imputation with a dataset. The usages of the S4 methods for signature `data.frame`, `mi.preprocessed`, and `mi` are described respectively below:

```
mi(object, info, n.imp = 3, n.iter = 30,
   R.hat = 1.1, max.minutes = 20, rand.imp.method = "bootstrap",
   preprocess = TRUE, run.past.convergence = FALSE,
   seed = NA, check.coef.convergence = FALSE,
   add.noise = noise.control())

mi(object, n.imp = 3, n.iter = 30,
   R.hat = 1.1, max.minutes = 20, rand.imp.method = "bootstrap",
   run.past.convergence = FALSE,
   seed = NA, check.coef.convergence = FALSE,
   add.noise = noise.control())

mi(object, info, n.iter = 30, R.hat = 1.1,
   max.minutes = 20, rand.imp.method = "bootstrap",
   run.past.convergence = FALSE, seed = NA)
```

- **object**: A data frame or an **mi** object that contains an incomplete dataset. **mi** only recognizes the special value **NA** as the missing data.
- **info**: The **mi.info** matrix returned by **mi.info()**. This matrix contains information about the data (e.g., number of cells that are missing in a variable, variable types, etc.), and some parameters that control the imputation procedure (see Section 2).
- **n.imp**: The number of independent imputation chains with different sets of starting values randomly drawn from the observed ones (see **rand.imp.method**). The default is 3 chains. A minimum of 2 chains are required in order to conduct the Gelman and Rubin convergence diagnostic (Gelman and Rubin 1992; Gelman, Carlin, Stern, and Rubin 2004).
- **n.iter**: The maximum number of imputation iterations. The default is 30 iterations.
- **R.hat**: The value of the \hat{R} statistic used as a convergence criterion. The default is 1.1 (Gelman and Rubin 1992; Gelman, Carlin, Stern, and Rubin 2004).
- **max.minutes**: The maximum number of minutes to operate the whole imputation process. The default is 20 minutes.
- **rand.imp.method**: The method used for random imputing starting values of the missing values. Currently, **mi()** only implements the **bootstrap** method: missing values are filled in with values that are randomly sampled from the observed data.
- **preprocess**: Default is **TRUE**. **mi()** will transform the variables that are not of standard distribution. These types of variable are **nonnegative**, **positive-continuous**, and **proportion**. The transformed variables then can be modeled using linear regression (see Section 3 for details).
- **run.past.convergence**: Default is **FALSE**, meaning **mi()** stops if the imputation is converged. If the value is **TRUE**, **mi()** will run until the values of either **n.iter** or **max.minutes** are reached even if the imputation is converged.
- **seed**: The random number seed. The default is **NA**.
- **check.coef.convergence**: Default is **FALSE**. **mi()** only checks the convergence of the means and standard deviations of the imputed values. If the value is **TRUE**, **mi()** also checks the convergence of the coefficients of imputation models.
- **add.noise**: A list of parameters for controlling the process of adding noise to **mi()** via **noise.control()**. This is to fill in the missing values with values that are randomly sampled from the observed ones. This step addresses the problem of collinearity that impedes appropriate imputation of missing data (see Section 3 for details).

mi() is a wrapper of several key components: the imputation information matrix, variable types and imputation models.

2.1. Imputation information matrix

mi.info() produces a matrix of imputation information that is needed to impute the missing data. After the information is extracted from a dataset, users can still alter the default model

specifications that are automatically created using this imputation information. Such a matrix of imputation information allows the users to have control over the imputation process. It contains the following information:

- **name:** The names of variables in the dataset.
- **imp.order:** A vector that records the order of each variable in the iterative imputation process. If such a variable is missing for all the observations (see **all.missing**), is an identification variable (see **is.ID**), and is not included (see **include**), the **imp.order** slot will record an **NA**.
- **nmis:** A vector that records the number of data points that are missing in each variable.
- **type:** A vector that contains the information of the variable types which are determined by **typecast()** (see Section 2).
- **var.class:** A vector that records the classes of the input variables.
- **level:** A list of the levels of the input variables.
- **include:** A vector of indicators that decide whether or not (**Yes/No**) to include a specific variable in an imputation process. If **include** is **No**, the variable will not show up either as a predictor or as a variable to be imputed.
- **is.ID:** A vector of indicators that determine whether or not (**Yes/No**) a specific variable is an identification (**ID**) variable. If a variable is detected as an **ID** variable, it will not be included in the imputation process; thus the **include** slot records a **No** value. **ID** variables are usually not problematic as dependent variables, since in most of the cases, they have no missing values. But when they are included in a model as predictors, they induce an unwanted order effect of the data into the model (unless the data is a repeated measure study and **ID** variables are treated as categorical variables). However, because **ID** variables are hard to detect, users should carefully check to see if all such variables have been detected.
- **all.missing:** A vector of indicators that identify whether or not (**Yes/No**) a variable is missing for all the observation. If the value is **TRUE**, such a variable will be excluded in the imputation process because it is not possible to impute sensible values. The **include** slot records a **No** value if **all.missing** is **TRUE**.
- **missing.index:** A vector that stores the index number of the missing units in a variable.
- **collinear:** A vector of indicators that shows whether or not (**Yes/No**) a variable is perfectly collinear with another variable. **mi.info()** uses **cor()** to compute the Pearson coefficients, a measure of the correlation (linear dependence) between two variables, of the data. If the Pearson coefficients are larger than 0.99999 (arbitrary chosen as the default in **mi**), **mi.info()** sets the value of the **collinear** slot to **TRUE**. Such a variable will be excluded in the imputation process (thus the **include** slot records a **No** value) if and only if these two variables have the same missing data pattern, meaning that they are missing in the same units.

- **imp.formula:** A vector of formulas that records the imputation formulas used in the imputation models. This formula represents the linear specification of the appropriate model. For instance, for a binary variable this formula represents the linear function of covariates that is set equal to the logit of the expectation of the response variable.
- **determ.pred:** The name of the corresponding correlated variable. This slot is `NULL` if there is no corresponding correlated variable as identified by `cor()`.
- **params:** A list of parameters to pass on to the imputation models.
- **other:** Other options. This is currently not used.

Users can alter the `mi.info` matrix using `update()`. For instance, if we have a variable x_1 in a dataset, and we do not want to include it in the imputation process, we can update the `include` slot of the `mi.info` matrix by:

```
R> info
```

	names	include	order	number.mis	all.mis	type	collinear
1	x1	Yes	1	40	No	continuous	No
2	x2	Yes	2	13	No	continuous	No
...							

```
R> info <- update(info, "include", list("x1" = FALSE))
R> info
```

	names	include	order	number.mis	all.mis	type	collinear
1	x1	No	NA	40	No	continuous	No
2	x2	Yes	1	13	No	continuous	No
...							

2.2. Variable types

mi handles eleven variable types. Within `mi()`, `mi.info()` uses `typecast()` to automatically identify eight different variable types; `mi.preprocess()` specifies the `log-continuous` type via transformation (see Section 3). The variable types that are not automatically identified by `typecast()` are `count` and `predictive-mean-matching` type.¹ These two types must be user-specified via `update()`. `typecast()` identifies variable types using the rules depicted in Figure 1.

The rules, which `typecast()` uses to identify each variable type, are listed as follows:

1. **fixed:** Any variable that contains a single unique value.
2. **binary:** Any variable that contains two unique values.

¹`predictive-mean-matching` is not really a variable type. We include it here to invoke `mi()` to fit a model using the predictive mean matching method (see Section 2)

3. **ordered-categorical**: Any variable that has the ordered attribute that is determined by `is.ordered()` in R. Or any numerical variable that has 3 to 5 unique values.
4. **unordered-categorical**: Any factor or character variable that is determined by `is.character()` or `is.factor()` in R. This type of variable often is not saved as a character or factor variable. Additionally, `typecast()` will identify a numeric unordered categorical variable as a continuous or an ordered categorical variable if users are not vigilant about identifying it. An unordered categorical variable, once is identified by `typecast()` or is specified by user, it is going to be imputed with a multinomial log-linear model (see Section 2) but is included in the imputation models of other variables as a factorized predictor (i.e., R will split this variable into the respective indicator variables).
5. **proportion**: Any numerical variable that has its values fall between 0 and 1, not including 0 and 1.
6. **positive-continuous**: Any numerical variable that is always positive and has more than 5 unique values.
7. **nonnegative**: Any numerical variable that is always nonnegative and has more than 5 unique values.
8. **continuous**: Any numerical variable that is modeled as continuous without transformation.
9. **log-continuous**: log-scaled continuous variable, specified by `mi.preprocess()` (see Section 3).
10. **count**: A user-specified variable type.
11. **predictive-mean-matching**: An user-specified variable type (see Section 2).

Once the variable type is determined by `typecast()`, the `type` information will be stored in the `mi.info` matrix. Nonetheless, users can alter this default judgment. For instance, if `riot` is the number of riots in a specific year, its values are very likely to fall between 0 and any positive integer. Hence, `typecast()` is going to identify `riot` as either **ordered-categorical**, **positive-continuous** or **nonnegative** type, depending on number of unique values it has and whether or not its values contains 0. You can alter this judgment by updating the `type` slot in a `mi.info` matrix as:

```
R> info
```

	names	include	order	number.mis	all.mis	type	correlated
1	riot	Yes	1	23	No	nonnegative	No
...							

```
R> info <- update(info, "type", list("riot" = "count"))
R> info
```

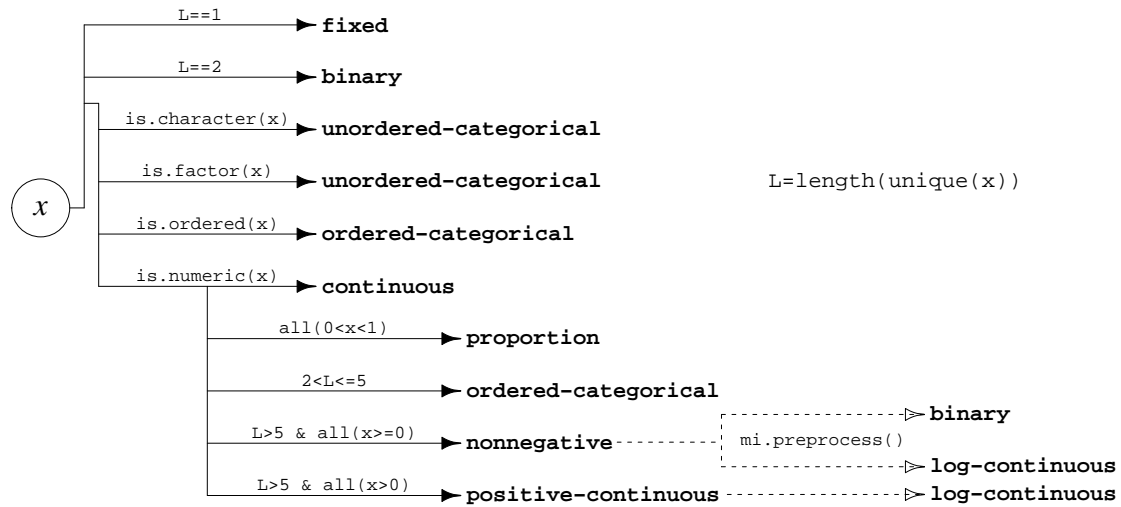


Figure 1: Illustration of the rules of `typecast()` to identify and classify different variable types. **mi** currently handles eleven variable types: `fixed`, `binary`, `unordered-categorical`, `ordered-categorical`, `proportion`, `positive-continuous`, `nonnegative`, `continuous`, `log-continuous`, `count`, and `predictive-mean-matching`. But **mi** can only automatically identify the first eight variable types. `mi.preprocess()` specifies `log-continuous` variable type via transformation. Users have to specify `count` and `predictive-mean-matching` variable types manually via `update()` or interactively via `mi.interactive()`.

```

names include order number.mis all.mis type correlated
1 riot Yes 1 23 No count No
...

```

2.3. Imputation models

By default, **mi** chooses the conditional models via `type.model()`, a function that determines which imputation models to use based on the variable types determined by `typecast()`. Table 1 lists the default regression models corresponding to variable types. `mi.fixed()` just copies the values from the observed one. `mi.categorical()` uses `multinom()` (multinomial log-linear model, Venables and Ripley 2002) to impute unordered categorical variables. **mi** uses `mi.continuous()` to impute `positive-continuous`, `nonnegative`, and `proportion` variable types.

`mi.continuous()`, `mi.binary()`, `mi.count()`, and `mi.polr()` fit Bayesian version of the generalized linear models (`bayesglm()` and `bayespolr()`, see Gelman, Jakulin, Pittau, and Su 2008) of **arm** (Gelman, Su, Yajima, Hill, Pittau, Kerman, and Zheng 2011). The Bayesian version of the generalized linear model that we use is different from the classical generalized linear model in that it adds a Student-*t* prior on the regression coefficients. Gelman, Jakulin, Pittau, and Su (2008) propose a new prior distribution for classical (nonhierarchical) logistic regression models, constructed by first scaling all nonbinary variables to have mean 0 and standard deviation 0.5, and then placing an independent Student-*t* prior distribution on the

Variable types	mi regression functions
binary	<code>mi.binary</code>
continuous	<code>mi.continuous</code>
count	<code>mi.count</code>
fixed	<code>mi.fixed</code>
log-continuous	<code>mi.continuous</code>
nonnegative	<code>mi.continuous</code>
ordered-categorical	<code>mi.polr</code>
unordered-categorical	<code>mi.categorical</code>
positive-continuous	<code>mi.continuous</code>
proportion	<code>mi.continuous</code>
predictive-mean-matching	<code>mi.pmm</code>

Table 1: List of **mi** regression functions, corresponding to variable types.

coefficients. As a default choice, they recommend the Cauchy distribution with center 0 and scale 2.5. At the present time, `mi()` does not allow users to alter the priors.

While this is a reasonably wide selection of models, it is still possible that none provide completely adequate fit for the data which could lead to improper imputation. Achieving appropriate fit can be particularly challenging when constraints exist in the data, when heteroskedasticity exists in a model, when multiple modes exist or a variety of other modeling challenges. To address this issue, **mi** offers an option to impute these data using the predictive mean matching method (Rubin 1987; Heitjan and Little 1991; Schenker and Taylor 1996). The predictive mean matching method (`mi.pmm()`) works in the following way. For each observation with a missing value on a given variable, we find the observation (from among those with observed values on that variable) with the closest predictive mean for that variable. The observed value from this “match” is then used as the imputed value. Currently, these predictions are obtained from `bayesglm()`. However, we plan to extend the predictive mean matching options in the future. This method can be problematic when rates of missingness are high or when the missing values fall outside the range of the observed data. We are continuing to develop more flexible imputation models to better address the issue of creating appropriate imputations.

3. Novel features

Our **mi** has some novel features that address some open issues in multiple imputation.

3.1. Bayesian models to address problems with separation

Logistic regression, and more generally, discrete data models, commonly suffer from the problem of separation. This problem occurs whenever the outcome variable is perfectly predicted by a predictor or a linear combination of the predictors. This can happen even with a modest number of predictors, particularly if the proportion of “successes” in the response variable is relatively close to 0 or 1. The risk of separation typically increases as the number of predictors increases. However, multiple imputation is generally strengthened by including many variables, which can help to impute more precisely and also may help to satisfy the miss-

mi functions	Bayesian functions
<code>mi.continuous()</code>	<code>bayesglm()</code> with <code>gaussian</code> family
<code>mi.binary()</code>	<code>bayesglm()</code> with <code>binomial</code> family (default uses <code>logit</code> link)
<code>mi.count()</code>	<code>bayesglm()</code> with <code>quasi-poisson</code> family (overdispersed poisson)
<code>mi.polr()</code>	<code>bayespolr()</code>

Table 2: Lists of Bayesian generalized linear models used in **mi** regression functions.

ing at random assumption. When imputing large-scale surveys to create public-use multiply imputed datasets, several hundred variables might need to be imputed. And it is unclear how or if we should start discarding subsets of variables from some or all of the conditional models. Separation problems can cause the chained equation algorithms to either fail or impute unreasonable values. Moreover, even without perfect separation, imposing priors on regression coefficients improves imputation in cases of near-separation and/or collinearity or near-collinearity of predictors (Gelman, Jakulin, Pittau, and Su 2008).

To address problems with separation, we have augmented our **mi** to allow for Bayesian version of the generalized linear models with Student-*t* prior distributions on regression coefficients (the default prior uses *t* distribution with center 0, degree of freedom 1 and scale 2.5). The models, as implemented in the functions `bayesglm()` and `bayespolr()`, automatically handle separation (Gelman, Jakulin, Pittau, and Su 2008). The corresponding imputation models are listed in Table 2.²

3.2. Imputing semi-continuous data with transformation

Semi-continuous data (`positive-continuous`, `nonnegative` and `proportion` variable types in **mi**) are typically not modeled in a reasonable way in other imputation software. The difficulty comes from the fact that these kinds of data have bounds or truncations and are not of standard distributions. Our algorithm models these data using transformations via `mi.preprocess()`. These transformations are automatically performed in `mi()` by setting the option `preprocess = TRUE` (which is the default).

For the `nonnegative` variable type, `mi.preprocess()` creates two ancillary variables. One is an indicator for which values of the `nonnegative` variable are greater than 0. The other ancillary variable takes the log of the original variable for any value that is greater than 0. For the `positive-continuous` variable type, `mi.preprocess()` takes the log of the variable. For the `proportion` variable type, `mi.preprocess()` does a logit transformation on the variable as $\text{logit}(x) = \log\left(\frac{x}{1-x}\right)$.

Figure 2 illustrates this transformation process. Users can transform the data back to the original scale using `mi.postprocess()`. This is implemented automatically in `mi.completed()` (see Section 4). For the `positive-continuous` variable (`x1`), it is going to be transformed back as $\widehat{x1} = \exp(x1.mi.log) \times x1.mi.ind$; for the `nonnegative` variable (`x2`), $\widehat{x2} = \exp(x2.mi.log)$; and for the `proportion` variable (`x3`), $\widehat{x3} = \text{logit}^{-1}(x3.mi.logit)$.

After the transformation, `mi()` uses `mi.continuous()` (Gaussian linear model) to impute these log transformed and logit transformed variables. Nonetheless, if the transformation is

²We are working on Bayesian version of multinomial models for unordered categorical variables. `mi()` now uses `mi.categorical()`, which uses `multinom()` (multinomial log-linear model, Venables and Ripley 2002), to handle with unordered categorical variables.

Original Dataset			Transformed Dataset			
x1	x2	x3	x1.mi.log	x1.mi.ind	x2.mi.log	x3.mi.logit
0.00	6.00	NA	NA	0.00	1.79	NA
NA	5.00	0.18	NA	NA	1.61	-1.49
6.00	10.00	0.54	1.79	1.00	2.30	0.15
19.00	NA	0.51	2.94	1.00	NA	0.04
0.00	NA	0.43	NA	0.00	NA	-0.27
5.00	NA	0.98	1.61	1.00	NA	4.00
NA	11.00	0.26	NA	NA	2.40	-1.06
10.00	NA	0.82	2.30	1.00	NA	1.54
18.00	5.00	0.16	2.89	1.00	1.61	-1.65
0.00	14.00	NA	NA	0.00	2.64	NA
...

Figure 2: Illustration of the way in which `mi.preprocess()` transforms the data of nonnegative (x1), positive-continuous (x2) and proportion (x3) variable types.

not enough to achieve a well-fitting model, we recommend that users utilize the predictive mean matching method as a work-around.

3.3. Imputing data with collinearity

mi can deal with two types of data with collinearity. One type is the perfect correlation of two variables (e.g., $x_1 = 10x_2 - 5$). The other type is for data with additive constraints across several variables (e.g., $x_1 = x_2 + x_3 + x_4 + x_5 + 10$).

Perfect correlation

In real datasets, a variable may appear multiple times or with different scale. For example, GDP per capita and GDP per capita in thousand dollars could both be in a dataset. For these variables, if the missingness pattern of these two variables is the same, **mi**() will include only one of the duplicated variables in the iterative imputation process. To impute data with such a perfect correlation, **mi**() will firstly identify such a pair of correlated variables via `mi.info()` and exclude one of them from the imputation process. If the absolute value of a Pearson coefficient of two variables is larger or equal to an arbitrary chosen threshold of 0.9999, these two variables are treated as correlated. Then **mi**() will use `mi.copy()` to impute the missing values of the excluded variable by duplicating values from the correlated variable. If for some reasons, the duplicated variables do not have the same missingness pattern (missing the same units), **mi**() keeps them in the iterative imputation process and utilizes the technique described in the next section (Section 3).

Additive constraints

General additive constraints can cause problems with the chained equation algorithm. However, they can be difficult to identify when we have missing data. Moreover, even if we identify such dependencies, if the variables in this grouping do not all have the same missing data pattern the solution is typically not obvious. This problem can exist either in deterministic situations (such as inclusion of all the items in a scale as well as the total scale score) or situations included in the model that by chance a subset of variables end up being functionally dependent on each other (i.e., each is a linear combination of the rest). Figure 3 displays a hypothetical example of a dataset with additive constraints. In this example, we have the number of female students (**female**), the number of male students (**male**) and the

Structured Correlated Dataset

class	total	female	male
1	66	NA	35
2	NA	27	23
3	76	37	NA
4	NA	31	NA
5	51	24	NA
6	73	39	34
7	NA	NA	39
8	NA	NA	NA
9	46	26	NA
10	59	NA	NA
...

Figure 3: Illustration of a dataset with additive constraints. In this dataset, `total = female + male`.

total number of students (`total`) in a given class. Hence, `total = female + male`. Such a problem could easily be dealt with if an investigator spots such a problem beforehand and takes out one of the variables. However, this problem could easily remain undetected, if such a problem of additive constraints exists across many variables without logically related and explicit variable names.

Computational issues can arise when more than one variable is missing. Take class 4 in Figure 3 for an example. `mi()` will first randomly assign a value for `male` in the class 4, say 20. Then `mi()` imputes `total` by regressing it on `male` and `female`. In this case, the value would be 51. Using the imputed value for `total`, the next imputation of `mi()` for `male` will be 20. Using this imputed value for `male`, the next imputed value for `total` will be 51. This situation will continue to repeat like this over and over. The result of this problem is that `mi()` will not be able to explore the entire response surface of the imputed variables.

To deal with this problem, we introduce an artificial set of prior distributions on the missing data into the iterative imputation process. The purpose is to create noise that breaks the deterministic structure to force `mi()` to explore more of the response surface of the imputed variables. At the same time, because the priors originate from the observed data, they also ensure that the imputed values do not deviate too far from the observation. `mi()` currently offers two options via `noise.control()`, each of which temporarily adds prior information to the model fits.

- Reshuffling noise: By default, `mi()` adds noise to the iterative imputation process by randomly imputing missing data for a given variable from the empirical marginal distribution. In other words, `mi()` imputes the missing data by sampling from the observed data. In every iteration, `mi()` decides whether or not to impute the missing data from the marginal distribution based on a random bernoulli variable q with a probability $p = \frac{K}{s}$, where s is the number of imputation iteration and K is specified by the user (the default is 1). If $q = 1$, `mi()` imputes the missing data with values from the observed data. Otherwise, it imputes missing data with values from the conditional models.

The influence of the noise gradually declines because p gradually decreases to the zero as the number of iterations increases. This means `mi()` eventually imputes the missing

data only from the conditional models. Hence, depending on the size of K (default is 1), users can control how much power they want the noise to insert into the iterative imputation process. The standard usage is as below:

```
R> IMP <- mi(data, add.noise = noise.control(method = "reshuffling",
+      K = 1))
```

- Fading empirical noise. In each iteration, `mi()` augments the data by `pct.aug = 10` percent (default) of the completed data by randomly adding new data that are drawn from the observed data. Hence the noise is added to all variables. Thus if a completed dataset has 250 data points, `mi()` will augment such a dataset with 25 new data points from the observed data of the complete case. The standard usage is as below:

```
R> IMP <- mi(data, add.noise = noise.control(method = "fading",
+      pct.aug = 10))
```

By default, `mi()` uses the reshuffling noise. If users have faith that their data have neither of the two correlation problems, they can choose not to add noise into the imputation process by specifying `mi(data, add.noise = FALSE, ...)`. By default, if any of the two methods of adding noise is used, `mi()` will run 20 more iterations (controlled by `post.run.iter`, default is 20) without adding any noise to mitigate the influence of the noise. To change the default number of iterations from 20 to 30, user simply runs:

```
R> IMP <- mi(data, add.noise = noise.control(post.run.iter = 30))
```

If `post.run.iter` is set to zero, `mi()` will not run any additional iteration to mitigate the influence of the noise. This is not recommended, though, users can still run additional iterations later by doing the following:

```
R> IMP <- mi(IMP)
```

3.4. Checking the convergence of the imputations

Our **mi** offers two ways to check the convergence of the multiple imputation procedure. By default, `mi()` monitors the mixing of each variable by the variance of its mean and standard deviation within and between different chains of the imputation. If the \hat{R} statistic is smaller than 1.1, (i.e., the difference of the within and between variance is trivial), the imputation is considered converged (Gelman, Carlin, Stern, and Rubin 2004). Additionally, by specifying `mi(data, check.coef.convergence = TRUE, ...)`, users can check the convergence of the parameters of the conditional models.

3.5. Model checking and other diagnostic using graphics

Model checking and other diagnostics are generally an important part of any statistical procedure. This is particularly important to imputation because the model used for imputation in general is not the same as the model used for the analysis. Yet, there is a noticeable dearth of such checks in the multiple imputation world. Thus imputations are, for the most part, a black box. This likely stems from uncertainty regarding how to assess the appropriateness of imputed values that are proxies for data points that are by definition unknown. Our **mi** addresses this problem with three strategies.

- Imputations are typically generated using models, such as regressions or multivariate distributions, which are fit to observed data. Thus the fit of these models to the observed data can be checked (Gelman, Mechelen, Verbeke, Heitjan, and Meulders 2005) using standard graphical diagnostics.
- Imputations can be checked using a standard of reasonability: the differences between observed and missing values, and the distribution of the completed data as a whole, can be checked to see whether they make sense in the context of the problem being studied (Abayomi, Gelman, and Levy 2008).

So far, **mi** only implements the first two solutions with various plotting functions. We demonstrate the usages of these functions in Section 4.

4. Example

In this Section, we demonstrate some basic steps of **mi** with an example.

4.1. A study of HIV-positive people in New York City

The CHAIN dataset included in **mi** is a subset of the Community Health Advisory and Information Network (CHAIN) study. This study is a longitudinal cohort study of people living with HIV in New York City and is conducted by Columbia University School of Public Health (Messerli, Lee, Abramson, Aidala, Chiasson, and Jessop 2003). The CHAIN cohort was recruited in 1994 from a large number of medical care and social service agencies serving HIV in New York City. Cohort members were interviewed up to 8 times through 2002. A total of 532 CHAIN participants completed at least one interview at either the 6th, 7th or 8th rounds of interview, and 508,444,388 interviews were completed respectively at rounds 6, 7 and 8 (CHAIN 2009). For simplicity, our analysis here discards the time aspect of the dataset and use only the 6th round of the survey. The dataset has 532 observations and has the following 8 variables:

- **h39b.W1**: Log of self reported viral load level, 0 represents undetectable level.
- **age.W1**: The respondent's age at time of interview.
- **c28.W1**: The respondent's family annual income. Values range from under USD 5,000 to USD 70,000 or over.
- **pcs.W1**: A continuous scale of physical health with a theoretical range between 0 and 100 (better health is associated with higher scale values).
- **mcs37.W1**: A dichotomous measure of poor mental health: 0 = No, 1 = Yes.
- **b05.W1**: Ordered interval for the CD4 count (the indicator of how much damage HIV has caused to the immune system).
- **haartadhere.W1**: A three-level-ordered variable: 0 = not currently taking highly active antiretroviral therapy (HAART), 1 = taking HAART nonadherent, 2 = taking HAART adherent.

To use the data, users must first load the **mi** package:³

```
R> library("mi")

Loading required package: MASS
Loading required package: nnet
Loading required package: car
...
Loading required package: arm
Loading required package: Matrix
Loading required package: lattice
...
Loading required package: lme4
...
Loading required package: abind

mi (Version 0.09-13, built: 2011-2-15)
```

Then load the CHAIN dataset in the memory:

```
R> data("CHAIN")
```

4.2. Setup

The first thing to do is to set up the imputation. As with most statistical procedures, one must start with some preliminary analysis to avoid trivial problems. When that is completed, two key steps must be done: choosing the conditional models and specifying the models.

Preliminary analysis is crucial in an iterative procedure such as multiple imputation that uses the chain equation algorithm. Users do not want simple mistakes that arise in the early stages to ruin the end result after a long iteration. In a small dataset, this may not be a serious issue, but for a large dataset, this may be costly. There are problems which **mi** automatically detects. But there are problems that are not possible to detect automatically by **mi**. For those problems that are difficult to detect, our **mi** will raise flags so that user can keep them in mind.

Display of missing data patterns

Users can get the glimpse of the data by looking at the missingness pattern.

```
R> missing.pattern.plot(CHAIN, clustered = FALSE)
```

Or simply type:

³The printout of the loaded information shows that **mi** depends upon on several R packages, including **MASS** and **nnet** (Venables and Ripley 2002), **car** (Fox and Weisberg 2011), **arm** (Gelman *et al.* 2011), **Matrix** (Bates and Maechler 2011), **lme4** (Bates, Maechler, and Bolker 2011), **R2WinBUGS** (Sturtz, Ligges, and Gelman 2005), **coda** (Plummer, Best, Cowles, and Vines 2006) and **abind** (Plate and Heiberger 2011). In the last line of the loaded information, R prints out the version number of **mi**. Users are welcome to report bugs or make suggestions to us with the attached version number.

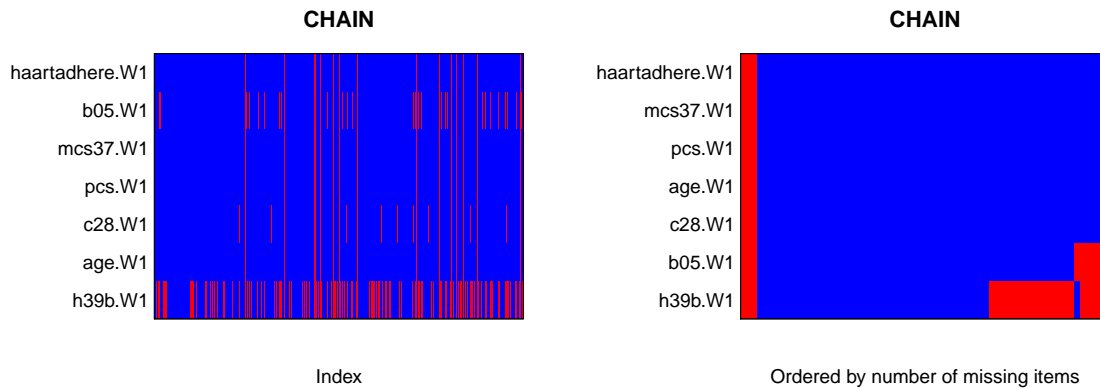


Figure 4: Missingness pattern plot. The observed values are plotted with blue and the missing values are in red. In the right panel, variables and cases are ordered by proportion missing and clustered by similar missingness pattern.

```
R> mp.plot(CHAIN, clustered = FALSE)
```

Figure 4 (left) shows the data matrix with observed values in blue and missing values in red. At this point it is difficult to detect anything, but we also have the option to order them by the missing data rates (the x -axis is the data index and the y -axis is the variable index) and to cluster them by the missingness pattern.

```
R> mp.plot(CHAIN, y.order = TRUE, x.order = TRUE, clustered = TRUE)
```

Figure 4 (right) reveals that `h39b.W1` variable has the highest missing rate followed by `b05.W1` and `c28.W1`. The other variables have missingness only for the observations that have missing data for all of the variables. When there exist observations with all variables missing, the user should either remove these observations (since they will not add any new information to the imputation procedure) or include more variables (with observed values for these observations) from the full dataset if these exist.

Identifying structural problems in the data and preprocessing

Before starting to impute the missing data, we can review some basic data information, which will feed into the imputation process, and determine whether or not we want to adjust this information.

```
R> info <- mi.info(CHAIN)
R> info
```

	names	include	order	number.mis	all.mis	type	collinear
1	h39b.W1	Yes	1	179	No	nonnegative	No
2	age.W1	Yes	2	24	No	positive-continuous	No
3	c28.W1	Yes	3	38	No	positive-continuous	No
4	pcs.W1	Yes	4	24	No	positive-continuous	No
5	mcs37.W1	Yes	5	24	No	binary	No
6	b05.W1	Yes	6	63	No	ordered-categorical	No
7	haartadhere.W1	Yes	7	24	No	ordered-categorical	No

By default, `mi.info()` prints out seven out of the fourteen categories of the `mi.info` matrix (see Section 2). We can see from this output that `h39b.W1`, `age.W1`, `c28.W1`, and `pcs.W1` are variable types that need special treatment (see Section 3 for data preprocessing and transformation).

So to address the variable types that `mi.info()` identifies as requiring special treatment, **mi** preprocesses the data via `mi.preprocess()` and may change the default judgement returned by `typecase()` (see Section 2 and Figure 2). `mi.preprocess` returns an S4 object `mi.preprocess` that stores the transformed data in the slot `data` and the new `mi.info` object in the slot `mi.info`.

```
R> CHAIN.new <- mi.preprocess(CHAIN)
R> attr(CHAIN.new, "mi.info")
```

	names	include	order	number.mis	all.mis	type	collinear
1	h39b.W1.mi.log	Yes	1	367	No	log-continuous	No
2	age.W1.mi.log	Yes	2	24	No	log-continuous	No
3	c28.W1.mi.log	Yes	3	38	No	log-continuous	No
4	pcs.W1.mi.log	Yes	4	24	No	log-continuous	No
5	mcs37.W1	Yes	5	24	No	binary	No
6	b05.W1	Yes	6	63	No	ordered-categorical	No
7	haartadhere.W1	Yes	7	24	No	ordered-categorical	No
8	h39b.W1.mi.ind	Yes	8	179	No	binary	No

The new information matrix shows that `h39b.W1`, `age.W1`, `c28.W1`, and `pcs.W1` have been transformed into new variables with different scales and types. Also, the transformed variables have been attached with new suffixes.

Specifying the conditional models

`mi()` chooses the conditional models based on the variable types that are determined by `typecast()` (see Section 2). By changing the variable types, `mi()` will choose different conditional models to fit the altered variables. For example, you can change the type of `h39b.W1` from `nonnegative` to `continuous` as:

```
R> info <- mi.info(CHAIN)
R> info
```

	names	include	order	number.mis	all.mis	type	collinear
1	h39b.W1	Yes	1	179	No	nonnegative	No
...							

```
R> info.upd <- update(info, "type", list("h39b.W1" = "continuous"))
R> info.upd
```

	names	include	order	number.mis	all.mis	type	correlated
1	h39b.W1	Yes	1	179	No	continuous	No
...							

By default, `mi()` assumes linearity between the outcomes and additive predictors.

```
R> info$imp.formula
```

```

                                     h39b.W1
"h39b.W1 ~ age.W1 + c28.W1 + pcs.W1 + mcs37.W1 + b05.W1 + haartadhere.W1"
                                     age.W1
"age.W1 ~ h39b.W1 + c28.W1 + pcs.W1 + mcs37.W1 + b05.W1 + haartadhere.W1"
                                     c28.W1
"c28.W1 ~ h39b.W1 + age.W1 + pcs.W1 + mcs37.W1 + b05.W1 + haartadhere.W1"
                                     pcs.W1
"pcs.W1 ~ h39b.W1 + age.W1 + c28.W1 + mcs37.W1 + b05.W1 + haartadhere.W1"
                                     mcs37.W1
"mcs37.W1 ~ h39b.W1 + age.W1 + c28.W1 + pcs.W1 + b05.W1 + haartadhere.W1"
                                     b05.W1
"b05.W1 ~ h39b.W1 + age.W1 + c28.W1 + pcs.W1 + mcs37.W1 + haartadhere.W1"
                                     haartadhere.W1
"haartadhere.W1 ~ h39b.W1 + age.W1 + c28.W1 + pcs.W1 + mcs37.W1 + b05.W1"
```

If you want to change the fitted formulas by adding interactions or add squared terms, you can alter the `imp.formula` slot of the `mi.info` matrix via `update()` or interactively via `mi.interactive()`:

```

R> info.upd <- update(info, "imp.formula", list("h39b.W1" =
+       "h39b.W1 ~ age.W1^2 + c28.W1*pcs.W1 + mcs37.W1 +
+       b05.W1 + haartadhere.W1"))
R> info.upd$imp.formula["h39b.W1"]
```

```

                                     h39b.W1
"h39b.W1 ~ age.W1^2 + c28.W1*pcs.W1 + mcs37.W1 + b05.W1 + haartadhere.W1"
```

4.3. Imputation

Once everything has been setup correctly, actual imputation is simple. However, there are still a few things users should check: the fit of the conditional models and convergence of the imputation algorithm. Diagnostic tools are integrated as parts of `mi()`, but decisions about how to use the diagnostic information must be made by the users. We will provide general guidelines here.

Iterative imputation based on the conditional model

`mi()` imputes the missing values based on the conditional models. That is it will draw values (that is, stochastically sample) from the fitted conditional distributions. As demonstrated in the previous sections, you can modify the `mi.info` object and pass it into `mi()` to alter these model settings. If no `mi.info` object is passed into `mi()`, `mi()` will call `mi.info()` internally and use the default setting. Although this is not recommended, we have made the defaults as reasonable as possible.

```

R> CHAIN.new <- mi.preprocess(CHAIN)
R> IMP <- mi(CHAIN.new)
```

```

Beginning Multiple Imputation ( Fri Jul 02 10:54:34 2010 ):
Iteration 1
Chain 1 : h39b.W1.mi.log* age.W1.mi.log* c28.W1.mi.log* pcs.W1.mi.log* mcs37.W1* b05.W1* haartadhere.W1* h39b.W1.mi.ind*
Chain 2 : h39b.W1.mi.log* age.W1.mi.log* c28.W1.mi.log* pcs.W1.mi.log* mcs37.W1* b05.W1* haartadhere.W1* h39b.W1.mi.ind*
Chain 3 : h39b.W1.mi.log* age.W1.mi.log* c28.W1.mi.log* pcs.W1.mi.log* mcs37.W1* b05.W1* haartadhere.W1* h39b.W1.mi.ind*
Iteration 2
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log* mcs37.W1* b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log* c28.W1.mi.log* pcs.W1.mi.log* mcs37.W1 b05.W1 haartadhere.W1* h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log* c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind*
...
Iteration 30
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1* b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1* b05.W1 haartadhere.W1 h39b.W1.mi.ind
Reached the maximum iteration, mi did not converge ( Wed Feb 09 16:49:30 2011 )
Run 20 more iterations to mitigate the influence of the noise...
Beginning Multiple Imputation ( Wed Feb 09 16:49:30 2011 ):
Iteration 1
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Iteration 2
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
...
Iteration 20
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
mi converged ( Wed Feb 09 16:50:06 2011 )

```

By default, `mi()` will perform reshuffling, and run 20 more iterations after the first `mi()` is finished (`add.noise = noise.control(K = 1, post.run.iter = 20)`). The star symbols attached to the variable names indicate that reshuffling is being implemented for that variable in that iteration. Before doing `mi`, if users want to use the `mi()` to transform the data, they can transform the data with their own design or use `mi.preprocess()` to do the job. Here, we use `mi.preprocess()` to transform the data before we starting the imputation process.

There are other options to specify number of iterations (`n.iter`), how long `mi()` should run (`max.minutes`), whether or not `mi` should continue when it converged (`run.past.convergence`), etc (see Section 2 or type `?mi` in the R console for details).

Checking the fit of conditional models and imputed values

If the fit of our imputation models to the observed data is poor, it is unlikely that we will impute reasonable values for the missing values even our data are truly missing at random. We can check this fit through the binned residuals plot for the observed data and through overlaid histograms comparing observed and imputed data. Moreover, if the missing at random assumption is not appropriate we may be able to detect that by comparing imputed values to observed values based on what we know about the science of the phenomenon being measured by the variables in our dataset. **mi** provides three different plots to visually inspect the fit of the conditional models.

Imputation may take some time to run, depending on the size of the data. Thus we suggest that users may want to check the fit of the conditional models (Gelman, Mechelen, Verbeke, Heitjan, and Meulders 2005; Abayomi, Gelman, and Levy 2008) by plotting the `mi` object (Figure 5) after a reasonable number of iterations rather than waiting for convergence. Furthermore, if working with a large sample size, it may also be helpful to diagnose the imputation procedure for a random sample from the full sample.

```
R> plot(IMP)
```

The first plot displays histograms of the observed (in blue color), the imputed (in red color) and the completed (observed plus imputed, in black color) values. The second is a binned

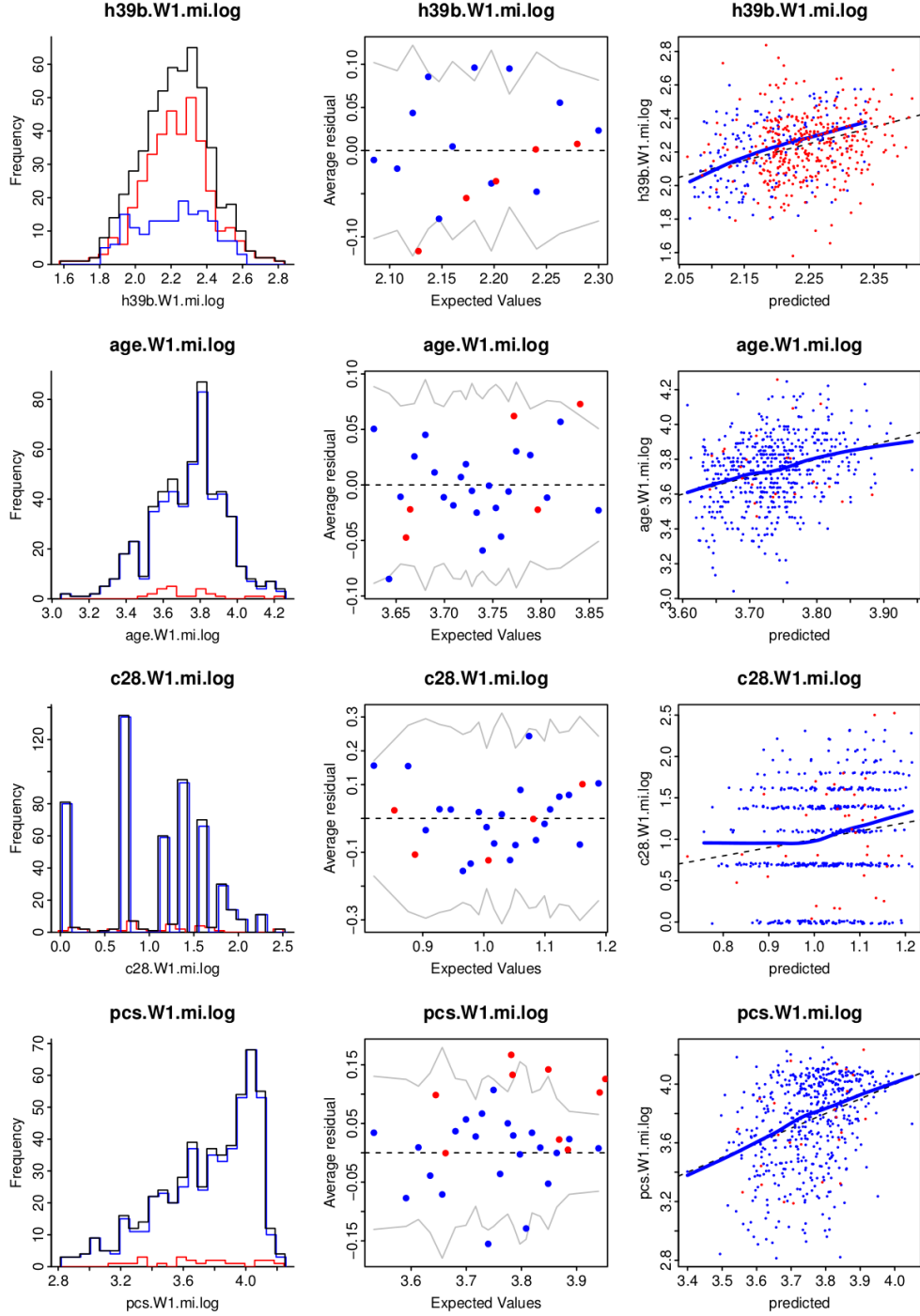


Figure 5: Diagnostic plots for checking the fit of the conditional imputation models. To save page space, only four out of the eight plots for each variable are displayed. The blue color is for the observed value and the red color is for the imputed one. By default, these values are plotted against an index number. Plotting against a variable that contains more information is a strongly recommended alternative. Fitted lowess curves are also plotted for the observed data. A small amount of random noise (jittering) is added to the points so that they do not fall on top of each other.

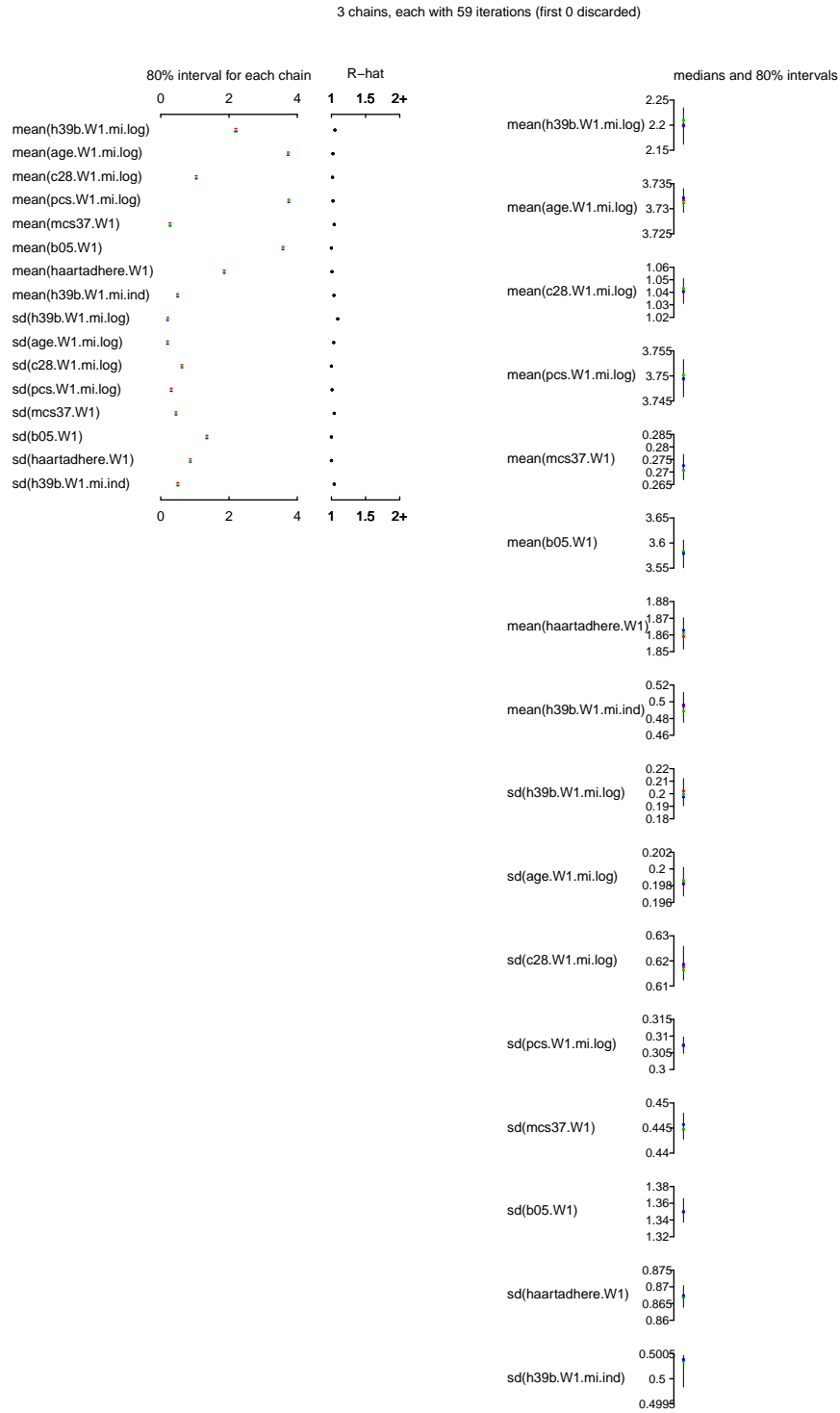


Figure 6: Plot of the summary of the mean and the standard deviation of each variable for the different chains of imputations. All the \hat{R} statistics are smaller than 1.1, indicating the imputation is converged.

residual plot that plots the average of residuals in bins against the expected values (Gelman, Goegebeur, Tuerlinckx, and Van Mechelen 2000). The third is a bivariate scatterplot that plots the observed or imputed values for each observation against the predicted values, overlaid with fitted lowess curves of the observed data (Cleveland 1979).

Figure 5 displays the selected variables using these four diagnostic plots. The histograms show that the imputed values are all within reasonable ranges and do not differ much from the observed values. The binned residual plots show that there is room for improvement on the imputation models of `h39b.W1.mi.log` and `pcs.W1.mi.log` as there are a number of residuals that fall outside of the 95% error bounds (the dotted lines with light color). Each point in a binned residual plot is the average of the points that fall in a given “bin” (interval of the variable on the x -axis) from a standard residual point. The bivariate scatterplot demonstrates that there is no significant difference between observed and imputed values.

If users discover a problem when accessing these plots and want to alter the model specification to fix it, they can fix the `mi.info` object via `update()` or they can perform transformations to their variables before feeding the dataset into the `mi` program.

Checking the convergence of the procedure

Checking the convergence of multiple imputation is still an open research question. By default, `mi()` checks the mean and standard deviation of each variable for different chains. It considers the imputation to have converged when the $\hat{R} < 1.1$ for all the parameters (Gelman, Carlin, Stern, and Rubin 2004). There is a `R.hat` option in `mi()` that allows users to adopt more stringent rule on checking convergence using the \hat{R} statistics (`mi(CHAIN, R.hat = 1)`). Users can also check the convergence of parameters of each conditional model by specifying `mi(CHAIN, check.coef.convergence = TRUE)`. Figure 6 shows that the \hat{R} value of each variable is smaller than 1.1 indicate that the imputation is converged.

```
R> plot(as.bugs.array(IMP@mcmc))
```

If the imputation is not converged or if conditional models seem to be fit reasonably but users may still want to run the imputation longer, users can do this by feeding the previous returned `mi` object into `mi()`. Imputation will continue from where it left off. If the previous `mi()` object is converged, you have to specify `run.past.convergence = TRUE` to force `mi()` to run for more iterations.

```
R> IMP <- mi(IMP, run.past.convergence = TRUE, n.iter = 10)
```

```
Beginning Multiple Imputation ( Wed Feb 09 16:51:21 2011 ):
Iteration 21
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Iteration 22
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
...
Iteration 38
Chain 1 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 2 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
Chain 3 : h39b.W1.mi.log age.W1.mi.log c28.W1.mi.log pcs.W1.mi.log mcs37.W1 b05.W1 haartadhere.W1 h39b.W1.mi.ind
mi converged ( Wed Feb 09 16:52:13 2011 )
```

4.4. Analysis

One of the nice features of multiply imputed data is that we can conduct analyses as if the data were complete. Results from an analysis performed on each dataset must then be combined in a sensible way, for instance by using formulas proposed by Rubin (1987).

Obtaining completed datasets

If the users prefer to perform separate data analyses for each dataset by themselves, they can easily extract the completed datasets from the `mi` object via `mi.completed()`. This will return a list that contains multiple datasets.

```
R> IMP.dat.all <- mi.completed(IMP)
```

They can extract just one dataset from a specific chain of imputations via `mi.data.frame()`.

```
R> IMP.dat <- mi.data.frame(IMP, m = 1)
```

`mi` also offers an option to output these multiply imputed datasets into files. Currently, `mi` only supports three data formats: `csv`, `dta`, and `table`. The default output data format is `csv`.

```
R> write.mi(IMP)
```

The output files shall be stored under the working directory. The file names will be `midata1.csv`, `midata2.csv`, `midata3.csv`, ..., and so on.

Pooling the complete case analysis on multiply imputed datasets

`mi()` facilitates the analysis process by providing functions that perform these separate analyses and then combine the separate estimates into one estimate and standard error. `mi` currently offers seven regression functions: `lm.mi()`, `glm.mi()`, `polr.mi()`, `bayesglm.mi()`, `bayespolr.mi()`, `lmer.mi()`, and `glmer.mi()`.

```
R> fit <- lm.mi(h39b.W1 ~ age.W1 + c28.W1 + pcs.W1 + mcs37.W1 +
+   b05.W1 + haartadhere.W1, IMP)
R> display(fit)
```

```
=====
Separate Estimates for each Imputation
=====
```

```
** Chain 1 **
lm(formula = formula, data = mi.data[[i]])
               coef.est coef.se
(Intercept)    14.78      1.46
age.W1         -0.06      0.02
c28.W1         -0.44      0.10
pcs.W1         -0.04      0.02
mcs37.W1        1.20      0.43
b05.W1         -0.99      0.14
haartadhere.W1 -1.52      0.22
---
n = 532, k = 7
residual sd = 4.36, R-Squared = 0.24
```

```

** Chain 2 **
lm(formula = formula, data = mi.data[[i]])
      coef.est coef.se
(Intercept)   14.11    1.47
age.W1        -0.07    0.02
c28.W1        -0.33    0.10
pcs.W1        -0.04    0.02
mcs37.W1       1.54    0.44
b05.W1        -1.03    0.15
haartadhere.W1 -0.88    0.22
---
n = 532, k = 7
residual sd = 4.37, R-Squared = 0.20

** Chain 3 **
lm(formula = formula, data = mi.data[[i]])
      coef.est coef.se
(Intercept)   15.93    1.47
age.W1        -0.11    0.02
c28.W1        -0.22    0.09
pcs.W1        -0.03    0.02
mcs37.W1       1.21    0.43
b05.W1        -1.11    0.15
haartadhere.W1 -1.03    0.22
---
n = 532, k = 7
residual sd = 4.38, R-Squared = 0.21

=====
Pooled Estimates
=====
lm.mi(formula = h39b.W1 ~ age.W1 + c28.W1 + pcs.W1 + mcs37.W1 +
      b05.W1 + haartadhere.W1, mi.object = IMP)
      coef.est coef.se
(Intercept)   14.94    1.81
age.W1        -0.08    0.04
c28.W1        -0.33    0.16
pcs.W1        -0.03    0.02
mcs37.W1       1.32    0.49
b05.W1        -1.05    0.16
haartadhere.W1 -1.14    0.45
---

```

Nonetheless, if users are running regression models that are not supported by **mi**, **mi** offers a function `mi.pooled()` that allows them to pool the regression estimates together with different chains. The following code demonstrates that by feeding `mi.pooled()` a list of coefficients

and standard deviations of these coefficients, `mi.pooled()` will produce the pooled estimates for the users.

```
R> m <- m(IMP)
R> coefs <- sds <- vector("list", m)
R> for(i in 1:m) {
+   dat <- mi.data.frame(IMP, i)
+   fit <- lm(h39b.W1 ~ c28.W1, data = dat, subset = mcs37.W1 == 1)
+   coefs[[i]] <- coef(fit)
+   sds[[i]] <- se.coef(fit)
+ }
R> mi.pooled(coefs, sds)

$coefficients
(Intercept)      c28.W1
   6.4413698  -0.2381554

$se
(Intercept)      c28.W1
   1.2055315    0.2931557
```

4.5. Validation

The validation step is still under construction and is not included in the current version. However, we present some ideas of the ways in which users can validate their results obtained from **mi**.

Sensitivity analysis

Multiple imputation is based on many assumptions about the conditional models. Thus it is natural to test how sensitive imputed values are to these assumptions. Since **mi** is extremely flexible about the model specification and also provides diagnostics to examine model fit, the user can check the sensitivity of the results from pooled analyses to changes in model specification within the subset of models that appear to be equally plausible based on the graphical diagnostics.

Cross validation

We can use cross-validation to explore robustness to violations of our structural assumptions. For instance, if we want to test the assumption of missing at random, after obtaining the completed dataset (original data plus imputed data) using **mi**, we can create missing values on these imputed datasets based on a missing at random missing data mechanism that mimics patterns of missingness actually found in the data and re-impute the missing data (Gelman, King, and Liu 1998). By comparing the imputed dataset before and after this test, we can assess how our procedure is likely to fair under this particular assumption of missing at random. Similar checks could be performed to assess performance of the procedure under the assumption of data not missing at random.

Compatibility check

We will use graphical diagnostics to assess the extent to which our conditional models fail to provide consistent information about the underlying joint distribution of the data and explore the extent to which such incompatibility might impact our results.

4.6. Interactive interface

mi has an interactive program where users do not have to type commands to perform multiple imputation. By calling `mi.interactive()` and giving it the data to be imputed, it will walk the users through all the necessary settings and steps as discussed in the previous sections.

```
R> data("CHAIN")
R> IMP <- mi.interactive("CHAIN")

-----
creating information matrix:
-----

done

-----

Would you like to:
-----

1: look at current setting
2: proceed to mi with current setting
3: change current setting
```

Selection:

Additionally, **migui** (Lee and Su 2010) offers a graphical user interface (GUI) of **mi** where users can do multiple imputation by clicking buttons. To call up the GUI, simply type the followings in the R console:

```
R> library("migui")
R> migui()
```

5. Conclusions and future plans

The major goal of **mi** is to make multiple imputation transparent and easy to use for the users. Here are four characteristics of the package that we believe are particularly valuable.

1. Graphical diagnostics of imputation models and convergence of the imputation process.
2. Use of Bayesian versions of regression models to handle the issue of separation.

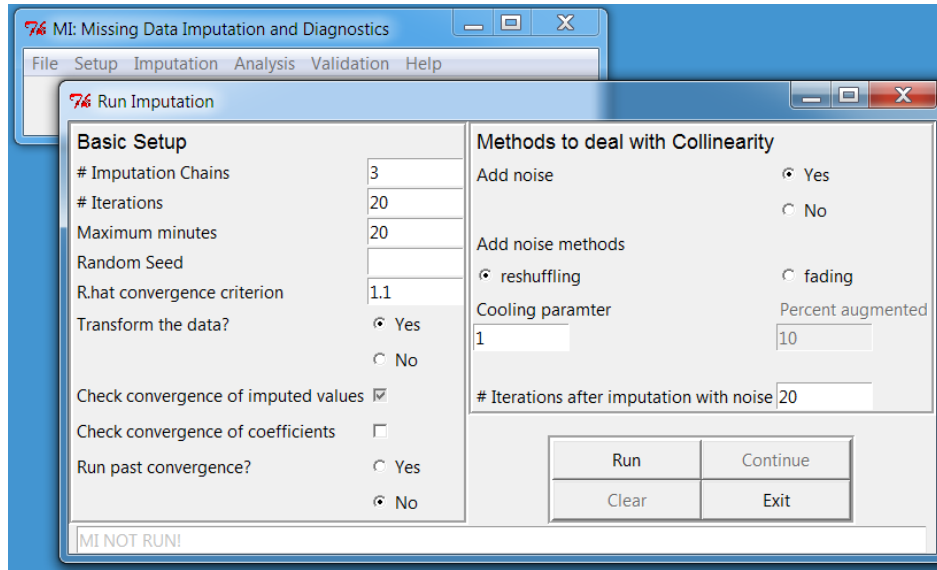


Figure 7: The screenshot of the graphical user interface of **mi**.

3. Imputation model specification is similar to the way in which you would fit a regression model in R.
4. Automatical detection of problematic characteristics of data such as high levels of collinearity across variables followed by either a fix or an alert to the user. In particular, **mi** adds noise into the imputation process to solve the problem of additive constraints.

As with many other software packages, **mi** is continually being augmented and improved. One caution with the current incarnation is that **mi** may take some time to converge with big datasets with a high rate of missingness across many variables. We are currently investigating approaches to increase the computational efficiency of the algorithm.

Another future direction includes expanding the functionality of **mi** to allow for imputation of time-series cross-sectional data, hierarchical or clustered data. Currently, it is only possible to include group or time indicators as predictors in the imputation process to capture the group-specific or time-specific aspect of missingness patterns. We would like to use multilevel models or approximations to these models to these types of data (Gelman and Hill 2007).

Finally, as discussed in Section 4, we will incorporate tools and functions to perform sensitivity analysis, cross-validation and compatibility checks for **mi**.

Afterward (December 1, 2011)

The bulk of this article was written in 2009 after the call for papers for this special issue. Since then, our software and others' have advanced in many ways. We are delighted to see that many of the novel features of **mi** described in our paper have since been independently developed and incorporated into other multiple imputation software. Our goal was and continues to be to use **mi** as an open-source vehicle for disseminating ideas for flexible, understandable, and

checkable missing data imputation. In particular, we are looking forward to seeing one of the important features of **mi** – model checking and cross validation after imputation – to be incorporated in other software, just as we will continue to take advantage of developments elsewhere in improving our programs. The synergy available from open-source software should be a general benefit.

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